

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/550,758
Source: P5/10
Date Processed by STIC: 10/7/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 10/07/2005

PATENT APPLICATION: US/10/550,758

TIME: 09:29:19

Input Set : A:\58049-00019.ST25.txt

Output Set: N:\CRF4\10072005\J550758.raw

```

2 <110> APPLICANT: Republic of National Fisheries Research and Development Institute
3     KIM, Young Ok
4     KIM, Han Woo
5     LEE, Jeong Ho
6     KIM, Kyung Kil
7     LEE, Jong Yun
8     KONG, In Soo
10 <120> TITLE OF INVENTION: Phytase produced from Citrobacter braakii
12 <130> FILE REFERENCE: 58049-00019
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/550,758
C--> 14 <141> CURRENT FILING DATE: 2005-09-23
14 <150> PRIOR APPLICATION NUMBER: PCT/KR2004/000680
15 <151> PRIOR FILING DATE: 2004-03-25
17 <150> PRIOR APPLICATION NUMBER: KR 10-2003-0018573
18 <151> PRIOR FILING DATE: 2003-03-25
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: KopatentIn 1.71
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1481
26 <212> TYPE: DNA
27 <213> ORGANISM: Citrobacter braakii YH-15
29 <220> FEATURE:
30 <221> NAME/KEY: MISC FEATURE
31 <222> LOCATION: (1134)..(1134)
32 <223> OTHER INFORMATION: n can be a, c, g or t
34 <400> SEQUENCE: 1
35 tagagtttga tcctggctca gattgaacgc tggcggcagg cctaacacat gcaagtcgaa 60
37 cggtagcaca gaggagcttg ctccttgggt gacgagtggc ggacgggtga gtaatgtctg 120
39 ggaaactgcc cgatggaggg ggataactac tggaaacggg agctaatacc gcataacgtc 180
41 gcaagaccaa agagggggac cttcgggcct cttgccatcg gatgtgcccc gatgggatta 240
43 gctagtaggt ggggtaacgg ctacactagg cgacgatccc tagctggtct gagaggatga 300
45 ccagccacac tggaaactgag acacgggtcca gactcctacg ggaggcagca gtggggaata 360
47 ttgcacaatg ggcgcaagcc tgatgcagcc atgccgcgtg tatgaagaag gccttcgggt 420
49 tgtaaaagtac tttcagcgag gaggaagggt ttgtggttaa taaccgcagc aattgacgtt 480
51 actcgcagaa gaagcaccgg ctaactccgt gccagcagcc gcggtataac ggagggtgca 540
53 agcggttaatc ggaattactg ggcgtaaagc gcacgcaggc ggtctgtcaa gtcggatgtg 600
55 aaatccccgg gctcaacctg ggaactgcac ccgaaactgg caggctagag tctttagtag 660
57 gggggtagaa ttccaggtgt agcggtgaaa tgcgtagaga tctggaggaa taccggtggc 720
59 gaaggcggcc ccctggacaa agactgcagc tcagggtgcga aagcgtgggg agcaaacagg 780
61 attagatacc ctggtagtcc acgccgtaaa cgatgtcgac ttggagggtt tgcccttgag 840
63 gcgtggcttc cggagctaac gcgttaagtc gaccgcctgg ggagtacggc cgcaagggtta 900
65 aaactcaaat gaattgacgg gggcccgcac aagcggtgga gcatgtggtt taattcgatg 960
67 caacgcgaag aaccttacct actcttgaca tccagagaaac ttagcagaga tgctttggtg 1020

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```

69 ccttcgggaa ctctgagaca ggtgctgcat ggctgctcgtc agctcgtggtt gtgaaatggtt 1080
W--> 71 ggggtaagtc cgcgaacgag cgcaaccctt atcctttggtt gccagcgggtt cggncgggaa 1140
73 ctcaaaggag actgccagtg ataaactgga ggaagggtggg gatgacgtca agtcatcatg 1200
75 gcccttacga gtagggctac acacgtgcta caatggcata tacaaagaga agcgacctcg 1260
77 cgagagcaag cggacctcat aaagtatgtc gtagtccgga ttggagtctg caactcgact 1320
79 ccatgaagtc ggaatcgcta gtaatcgtgg atcagaatgc cacggtgaat acgttccccg 1380
81 gccttgtaga caccgcccgt cacaccatgg gagtgggttg caaaagaagt aggtagctta 1440
83 accttcggga gggcgcttac ctctttggat tcagatgggg a 1481
86 <210> SEQ ID NO: 2
87 <211> LENGTH: 10
88 <212> TYPE: PRT
89 <213> ORGANISM: Citrobacter braakii YH-15
91 <400> SEQUENCE: 2
92 Glu Glu Gln Asn Gly Met Lys Leu Glu Arg
93 1 5 10
96 <210> SEQ ID NO: 3
97 <211> LENGTH: 12
98 <212> TYPE: PRT
99 <213> ORGANISM: Escherichia coli
101 <400> SEQUENCE: 3
102 Ser Glu Pro Glu Leu Lys Leu Glu Asn Ala Val Val
103 1 5 10
106 <210> SEQ ID NO: 4
107 <211> LENGTH: 15
108 <212> TYPE: PRT
109 <213> ORGANISM: Aspergillus ficuum
111 <400> SEQUENCE: 4
112 Phe Ser Tyr Gly Ala Ala Ile Pro Gln Ser Thr Gln Glu Lys Gln
113 1 5 10 15
116 <210> SEQ ID NO: 5
117 <211> LENGTH: 15
118 <212> TYPE: PRT
119 <213> ORGANISM: Bacillus sp.
121 <220> FEATURE:
122 <221> NAME/KEY: MISC_FEATURE
123 <222> LOCATION: (12)..(12)
124 <223> OTHER INFORMATION: Xaa can be any natural amino acid
126 <400> SEQUENCE: 5
W--> 127 Ser Asp Pro Tyr His Phe Thr Val Asn Ala Ala Xaa Glu Thr Glu
128 1 5 10 15
131 <210> SEQ ID NO: 6
132 <211> LENGTH: 1302
133 <212> TYPE: DNA
134 <213> ORGANISM: Citrobacter braakii YH-15
136 <220> FEATURE:
137 <221> NAME/KEY: gene
138 <222> LOCATION: (1)..(1302)
139 <223> OTHER INFORMATION: phytase gene
141 <400> SEQUENCE: 6

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```

142 atgagtacat tcatcattcg tttattaatt ttttctctct tatgcggttc tttctcaata 60
144 catgctgaag agcagaacgg catgaaactg gagcgggttg tgatagttag ccgtcatgga 120
146 gtaagagcac ctacgaagtt cactccaata atgaaagatg tcacacccga ccaatggcca 180
148 caatgggatg tgccggttagg atggctaact cctcgtgggg gagaacttgt ttctgaatta 240
150 ggtcagtatc aacgtttatg gttcacaagc aaagggtctgt tgaataatca aacgtgcccc 300
152 tctccagggc aggttgctgt tattgcagac acggatcaac gcacccgtaa aacgggtgag 360
154 gcgtttctgg ctgggttagc accaaaaatgt caaattcaag tgcattatca gaaggatgaa 420
156 gaaaaaaatg atcctctttt taatccggta aaaatgggga aatgttcgtt taacacattg 480
158 aagggttaaaa acgctattct ggaacggggc ggaggaaata ttgaactgta taccacaacgc 540
160 tatcaatctt catttcggac cctggaaaat gttttaaatt tctcacaatc ggagacatgt 600
162 aagactacag agaagtctac gaaatgcaca ttaccagagg ctttaccgtc tgaatttaag 660
164 gtaactcctg acaacgtatc attacctggt gcctggagtc tttcttccac gctgactgag 720
166 atatttctgt tgcaagagggc ccagggaatg ccacaggtag cctgggggag tattacggga 780
168 gaaaaagaat ggagagattt gttaaagtct cataacgctc agtttgatct ttgcaaaga 840
170 actccagaag ttgcccgtag tagggccaca ccattactcg atatgataga cactgcatta 900
172 ttgacaaatg gtacaacaga aaacaggtat ggcataaaat tacccgatc tctgttgttt 960
174 attgctggtc atgataccaa tcttgcaaat ttaagcgggg ctttagatct taagtggctg 1020
176 ctgcccgtc aacccgataa taccctcct ggtggggagc ttgtattcga aaagtggaaa 1080
178 agaaccagtg ataatacggg ttgggttcag gtttcatttg tttatcagac gctgagagat 1140
180 atgagggata ttcaaccgtt gtcgtagaa aaacctgctg gaaaagttga tttaaaatta 1200
182 attgcatgtg aagagaaaaa tagtcaggga atgtgttcgt taaaagttt ttccaggctc 1260
184 attaaggaaa ttgcggtgcc agagtgtgca gttacggaat aa 1302

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187 <210> SEQ ID NO: 7

188 <211> LENGTH: 433

189 <212> TYPE: PRT

190 <213> ORGANISM: Citrobacter braakii YH-15

192 <220> FEATURE:

193 <221> NAME/KEY: PEPTIDE

194 <222> LOCATION: (1)..(433)

195 <223> OTHER INFORMATION: phytase

197 <400> SEQUENCE: 7

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198 Met Ser Thr Phe Ile Ile Arg Leu Leu Ile Phe Ser Leu Leu Cys Gly
199 1 5 10 15
201 Ser Phe Ser Ile His Ala Glu Glu Gln Asn Gly Met Lys Leu Glu Arg
202 20 25 30
204 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Phe Thr
205 35 40 45
207 Pro Ile Met Lys Asp Val Thr Pro Asp Gln Trp Pro Gln Trp Asp Val
208 50 55 60
210 Pro Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Val Ser Glu Leu
211 65 70 75 80
213 Gly Gln Tyr Gln Arg Leu Trp Phe Thr Ser Lys Gly Leu Leu Asn Asn
214 85 90 95
216 Gln Thr Cys Pro Ser Pro Gly Gln Val Ala Val Ile Ala Asp Thr Asp
217 100 105 110
219 Gln Arg Thr Arg Lys Thr Gly Glu Ala Phe Leu Ala Gly Leu Ala Pro
220 115 120 125
222 Lys Cys Gln Ile Gln Val His Tyr Gln Lys Asp Glu Glu Lys Asn Asp
223 130 135 140

```

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```

225 Pro Leu Phe Asn Pro Val Lys Met Gly Lys Cys Ser Phe Asn Thr Leu
226 145 150 155 160
228 Lys Val Lys Asn Ala Ile Leu Glu Arg Ala Gly Gly Asn Ile Glu Leu
229 165 170 175
231 Tyr Thr Gln Arg Tyr Gln Ser Ser Phe Arg Thr Leu Glu Asn Val Leu
232 180 185 190
234 Asn Phe Ser Gln Ser Glu Thr Cys Lys Thr Thr Glu Lys Ser Thr Lys
235 195 200 205
237 Cys Thr Leu Pro Glu Ala Leu Pro Ser Glu Phe Lys Val Thr Pro Asp
238 210 215 220
240 Asn Val Ser Leu Pro Gly Ala Trp Ser Leu Ser Ser Thr Leu Thr Glu
241 225 230 235 240
243 Ile Phe Leu Leu Gln Glu Ala Gln Gly Met Pro Gln Val Ala Trp Gly
244 245 250 255
246 Arg Ile Thr Gly Glu Lys Glu Trp Arg Asp Leu Leu Ser Leu His Asn
247 260 265 270
249 Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
250 275 280 285
252 Ala Thr Pro Leu Leu Asp Met Ile Asp Thr Ala Leu Leu Thr Asn Gly
253 290 295 300
255 Thr Thr Glu Asn Arg Tyr Gly Ile Lys Leu Pro Val Ser Leu Leu Phe
256 305 310 315 320
258 Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Ser Gly Ala Leu Asp
259 325 330 335
261 Leu Lys Trp Ser Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
262 340 345 350
264 Glu Leu Val Phe Glu Lys Trp Lys Arg Thr Ser Asp Asn Thr Asp Trp
265 355 360 365
267 Val Gln Val Ser Phe Val Tyr Gln Thr Leu Arg Asp Met Arg Asp Ile
268 370 375 380
270 Gln Pro Leu Ser Leu Glu Lys Pro Ala Gly Lys Val Asp Leu Lys Leu
271 385 390 395 400
273 Ile Ala Cys Glu Glu Lys Asn Ser Gln Gly Met Cys Ser Leu Lys Ser
274 405 410 415
276 Phe Ser Arg Leu Ile Lys Glu Ile Arg Val Pro Glu Cys Ala Val Thr
277 420 425 430
279 Glu

```

282 <210> SEQ ID NO: 8

283 <211> LENGTH: 30

284 <212> TYPE: DNA

285 <213> ORGANISM: Artificial Sequence

287 <220> FEATURE:

288 <223> OTHER INFORMATION: primer for the detection of phytase gene

290 <400> SEQUENCE: 8

291 gargarcaga ayggyatgaa actggarcgy

30

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1134
Seq#:5; Xaa Pos. 12

VERIFICATION SUMMARY

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Input Set : A:\58049-00019.ST25.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1080

L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0